>SAK nucleotide (SEQ I D NO: 1)

ATGGCGACCTGCATCGGGGAGAAGATCGAGGATTTTAAAGTTGGAAATCTGC TTGGTAAAGGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATTCACACTGGT TTGGAAGTTGCAATCAAAATGATAGATAAGAAAGCCATGTACAAAGCAGGA ATGGTACAGAGAGTCCAAAATGAGGTGAAAATACATTGCCAATTGAAACATC CTTCTATCTTGGAGCTTTATAACTATTTTGAAGATAGCAATTATGTGTATCTG GTATTAGAAATGTGCCATAATGGAGAAATGAACAGGTATCTAAAGAATAGAG TGAAACCCTTCTCAGAAAATGAAGCTCGACACTTCATGCACCAGATCATCAC AGGGATGTTGTATCTTCATTCTCATGGTATACTACACCGGGACCTCACACTTT CTAACCTCCTACTGACTCGTAATATGAACATCAAGATTGCTGATTTTGGGCTG GCAACTCAACTGAAAATGCCACATGAAAAGCACTATACATTATGTGGAACTC CTAACTACATTTCACCAGAAATTGCCACTCGAAGTGCACATGGCCTTGAATCT GATGTTTGGTCCCTGGGCTGTATGTTTTATACATTACTTATCGGGAGACCACC CTTCGACACTGACACAGTCAAGAACACATTAAATAAAGTAGTATTGGCAGAT TATGAAATGCCATCTTTTTTGTCAATAGAGGCCAAGGACCTTATTCACCAGTT ACTTCGTAGAAATCCAGCAGATCGTTTAAGTCTGTCTTCAGTATTGGACCATC CTTTTATGTCCCGAAATTCTTCAACAAAAGTAAAGATTTAGGAACTGTGGA AGACTCAATTGATAGTGGGCATGCCACAATTTCTACTGCAATTACAGCTTCTT CCAGTACCAGTATAAGTGGTAGTTTATTTGACAAAAGAAGACTTTTGATTGGT CAGCCACTCCCAAATAAAATGACTGTATTTCCAAAGAATAAAAGTTCAACTG ATTTTTCTTCTCAGGAGATGGAAACAGTTTTTATACTCAGTGGGGAAATCAA GAAACCAGTAATAGTGGAAGGGGAAGAGTAATTCAAGATGCAGAAGAAGG CCACATTCTCGATACCTTCGTAGAGCTTATTCCTCTGATAGATCTGGCACTTCT AATAGTCAGTCTCAAGCAAAAACATATACAATGGAACGATGTCACTCAGCAG AAATGCTTTCAGTGTCCAAAAGATCAGGAGGAGGTGAAAATGAAGAGAGGT ACTCACCCACAGACAACAATGCCAACATTTTTAACTTCTTTAAAGAAAAGAC ATCCAGTAGTTCTGGATCTTTTGAAAGACCTGATAACAATCAAGCACTCTCCA ATCATCTTTGTCCAGGAAAAACTCCTTTTCCATTTGCAGACCCGACACCTCAG GAAAAACTACTGAATATGACAGCATCAGCCCAAACCGGGACTTCCAGGGCCA TCCAGATTTGCAGAAGGACACATCAAAAAATGCCTGGACTGATACAAAAGTC AAAAAGAACTCTGATGCTTCTGATAATGCACATTCTGTAAAACAGCAAAATA CCATGAAATATATGACTGCACTTCACAGTAAACCTGAGATAATCCAACAAGA ATGTGTTTTTGGCTCAGATCCTCTTTCTGAACAGAGCAAGACTAGGGGTATGG AGCCACCATGGGGTTATCAGAATCGTACATTAAGAAGCATTACATCTCCGTT GGTTGCTCACAGGTTAAAACCAATCAGACAGAAAACCAAAAAGGCTGTGGTG AGCATACTTGATTCAGAGGAGGTGTGTGTGGAGCTTGTAAAGGAGTATGCAT CTCAAGAATATGTGAAAGAAGTTCTTCAGATATCTAGTGATGGAAATACGAT CACTATTTATTCCAAATGGTGGTAGAGGTTTTCCTCTTGCTGATAGACCAC CCTCACCTACTGACAACATCAGTAGGTACAGCTTTGACAATTTACCAGAAAA ATACTGGCGAAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTAAGATCTA AATCTCCCAAAATCACTTATTTTACAAGATATGCTAAATGCATTTTGATGGAG AATTCTCCTGGTGCTGATTTTGAGGTTTGGTTTTATGATGGGGTAAAAATACA CAAAACAGAAGATTTCATTCAGGTGATTGAAAAGACAGGGAAGTCTTACACT TTAAAAAGTGAAAGTGAAGTTAATAGCTTGAAAGAGGAGATAAAAATGTAT

ATGGACCATGCTAATGAGGGTCATCGTATTTGTTTAGCACTGGAATCCATAAT
TTCAGAAGAGGAAAACTAGGÁGTGCTCCCTTTTTCCCAATAATCATA
GGAAGAAAACCTGGTAGTACTAGTTCACCTAAGGCCTTATCACCTCCTCCT
TGTGGATTCAAATTACCCAACGAGGAGATAGAGCATCCTTATCAACAGAATGGTC
ATGCATAGTGCTGCTTCTCCAACACCAGGCACCAATCCTTAATCCCTCTATGGT
TACAAATGAAGGACTTGGTCTTACAACTACAGCTTCTGGAACAGACATCCTT
CTAATAGTCTAAAAGATTGTCTTCCTAAATCAGCACAACTTTTGAAATCTGTT
TTTTGTGAAAAATGTTGGTTGGGCTACACAGTTAACTAGTGGAGCTGTGTGGGT
TCAGTTTAATGATGGGTCCCAGTTGGTTGTGCAGGCAGGAGTGTCTTCTATCA
GTTATACCTCACCAAATGGTCAAACAACTAGGTATTGGAGAAAATGAAAAATT
ACCAGACTACATCAAACAAGAAATTACAGTGTCTTCTCCATCCTTTTGATGT
TTTCTTAATCCGACTCCTAATTTTCATTGA

>SAK amino acid seq. (SEQ ID NO:2)

[MATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHTGLEVAIKMIDKKAMYKAGMVORVONEVKIHCOLKHP

 ${\tt SILELYNYFEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHQIITGMLYLHSHGILHRDLTLS}$

NLLLTRNMNIKIADFGLATQLKMPHEKHYTLCGTPNYISPEIATRSAHGLESDVW SLGCMFYTLLIGRPP

FDTDTVKNTLNKVVLADYEMPSFLSIEAKDLIHQLLRRNPADRLSLSSVLDHPFM SRNSSTKSKDLGTVE

DSIDSGHATISTÄITASSSTSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSG DGNSFYTOWGNO

ETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSNSQSQAKTYTMERCHSAEM LSVSKRSGGGENEERY

SPTDNNANIFNFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTETV OOWFGNLOINAHLR

KTTEYDSISPNRDFQGHPDLQKDTSKNAWTDTKVKKNSDASDNAHSVKQQNTM KYMTALHSKPEIIQQEC

VFGSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKTKKAVVSILD SEEVCVELVKEYASO

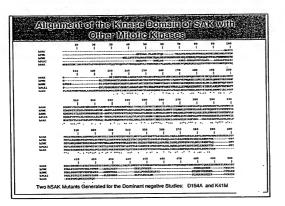
EYVKEVLQISSDGNTTTTYYPNGGRGFPLADRPPSPTDNISRYSFDNLPEKYWRKY OYASRFVOLVRSKS

PKITYFTRYAKCILMENSPGADFEVWFYDGVKIHKTEDFIQVIEKTGKSYTLKSES EVNSLKEEIKMYMD

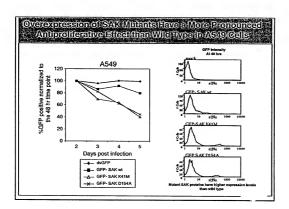
 ${\bf HANEGHRICLALESIISEE} {\bf EERKTRSAPFFPIIIGRKPGSTSSPKALSPPPSVDSNYPTR} \\ {\bf DRASFNRMVMH} \\ {\bf TRASFNRMVMH} \\ {\bf TRASFNRMVMMH} \\ {\bf$

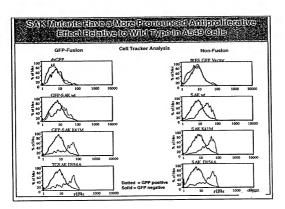
 ${\tt SAASPTQAPILNPSMVTNEGLGLTTTASGTDISSNSLKDCLPKSAQLLKSVFVKNV}\\ {\tt GWATQLTSGAVWVQ}$

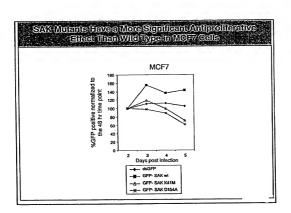
FNDGSQLVVQAGVSSISYTSPNGQTTRYGENEKLPDYIKQKLQCLSSILLMFSNPTPNFH

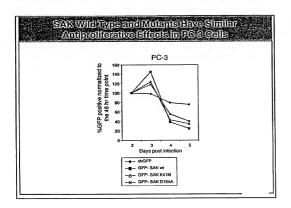


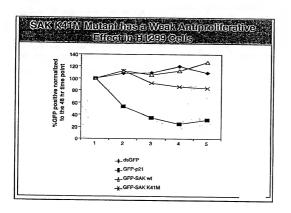
Dominant negative studies								
Wt								
GFP fusion	+	+	++	+/-	+/-	+/-	+/-	
IRES GFP	+	+		+/-	nd	+/-	nd	
K41M								
GFP fusion	++	++	++	+	+/-	+/-	+/-	
IRES GFP	++	++	++	+	nd	+/-	nd	
D154A								
GFP fusion	++	nd	++	+	+/-	+/-	+/-	
IRES GFP	++	nd	++	+	nd	+/-	nd	
Antisense: Hela		A549	9	H1299				
+	-	+	1-	+/-				

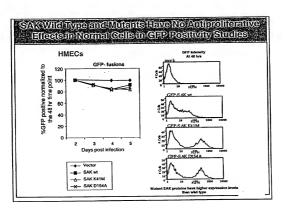


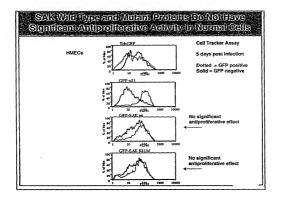


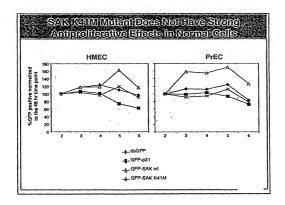












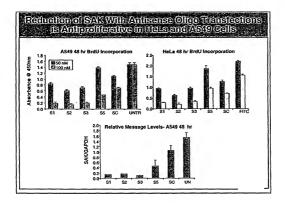
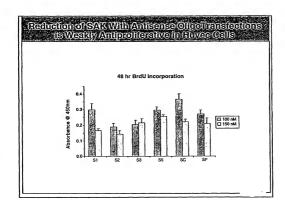
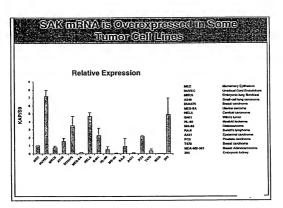


Figure 13





SANK Summery

Identification

Proteomics- Chk2 interacting protein

Functional Studies

- <u>Dominant Negative Studies</u>

 Mutant SAK has a much stronger antiproliferative phenotype than the wild type SAK in tumor cells while neither wild type or mutant SAK is antiproliferative in normal cells.

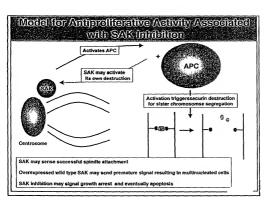
 The higher expression level of the mutant SAK relative to wild type makes it difficult of validate SAK only by the dominant negative strategy

Antisense Studies

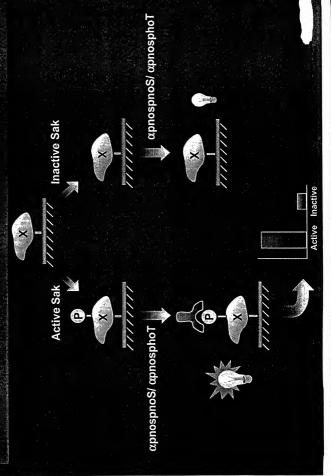
Preliminary studies suggests that inhibition of SAK mRNA with antisense oligos is antiproliferative in A549 and Hela cells

Literature

 Strong supporting literature shows antisense reduction of mouse SAK is antiproliferative and that the mouse SAK knockout results in increased cell cycle arrest and apoptosis



Biochemical assay for Sak kinase activity



Protocol for Sak Autophosphorylation Assaw

Bind Sak from E. coli lysates to Ni-NTA agarose O/N at 4°C



25 mM β-glycerol phosphate, 1 mM NaF, 1 mM Na₃VO₄, 1 mM NaPyP, 10% glycerol Wash Ni-NTA with lysis buffer (20 mM Hepes,pH 7.2, 0.5 M NaCl, 0.5% Tween-20,



Wash Ni-NTA with kinase buffer (20 mM MOPS, pH 7.2, 25 mM β-glycerol phosphate, 5 mM EGTA, 1 mM Na₃VO₄)



Add 10 μL of labeling mix (20 mM MgCl₂, 2 mM MnCl₂, 0.2 mM ATP, Resuspend resin-bound Sak in 10 µL kinase buffer 0.5 μ Ci/ μ L γ -³2P ATP in kinase buffer ncubate at 30°C, 15 min.

Autophosphorylation Activity of Sak Produced in *E. coli*i

